

## SEQUENCE LISTING

&lt;110&gt; ARES TRADING S.A.

&lt;120&gt; Leucine rich repeat containing protein

&lt;130&gt; P036769WO

&lt;150&gt; GB 0403142.3

&lt;151&gt; 2004-02-12

&lt;160&gt; 50

&lt;170&gt; SeqWin99, version 1.02

&lt;210&gt; 1

&lt;211&gt; 496

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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&lt;211&gt; 166

&lt;212&gt; PRT

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Phe Thr Gly Ile Met Thr Asn Ala Ser Arg Lys Ser Asn Ile Leu Phe
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Asn Ser Glu Cys Gln Trp Asn Glu Tyr Ile Leu Thr Asn Cys Ser Phe
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Thr Gly Lys Cys Asp Ile Pro Val Asp Ile Ser Gln Thr Ala Ala Thr
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Val Asp Val Ser Phe Asn Phe Phe Arg Val Leu Leu Gln Ser His Thr
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Lys Lys Glu Glu Trp Lys Ile Lys His Leu Asp Leu Ser Asn Asn Leu
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Ile Ser Lys Ile Thr Leu Ser Pro Phe Ala Tyr Leu His Ala Leu Glu
100                      105                      110

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Val Leu Asn Leu Ser Asn Asn Ala Ile His Ser Leu Ser Leu Asp Leu
115                      120                      125

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Leu Ser Pro Lys Ser Ser Trp Val Lys Arg His Arg Ser Ser Phe Arg  
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Asn Arg Phe Pro Leu Leu Lys Val Leu Ile Leu Gln Arg Asn Lys Leu  
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Ser Asp Thr Pro Lys Gly  
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Phe Lys Asp Leu Lys Lys Leu Gln  
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 20 25 30

Asn Trp Gln Cys Asp Asp Ser Val Ala Val Phe Gln Asn Phe Ile Ser

35 40 45

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<212> PRT
<213> Homo sapiens

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Asn Ser Glu Cys Gln Trp Asn Glu Tyr Ile Leu Thr Asn Cys Ser Phe
35 40 45

Thr Gly Lys Cys Asp Ile Pro Val Asp Ile Ser Gln Thr Ala Ala Thr
50 55 60

Val Asp Val Ser Phe Asn Phe Phe Arg Val Leu Leu Gln Ser His Thr
65 70 75 80

Lys Lys Glu Glu Trp Lys Ile Lys His Leu Asp Leu Ser Asn Asn Leu
85 90 95

Ile Ser Lys Ile Thr Leu Ser Pro Phe Ala Tyr Leu His Ala Leu Glu
100 105 110

Val Leu Asn Leu Ser Asn Asn Ala Ile His Ser Leu Ser Leu Asp Leu
115 120 125

Leu Ser Pro Lys Ser Ser Trp Val Lys Arg His Arg Ser Ser Phe Arg
130 135 140

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Met	Tyr	Lys	Thr	His	Leu	Glu	Asn	Ala	Ser	Asp	Thr	Asp	Arg	Ser	Glu	
785					790					795					800	



Gly Leu Ser Pro Trp Pro Arg Ser Pro Gly Asn Ser Pro Leu Gly Asp  
805 810 815

Glu Phe Pro Gly Met Phe Thr Tyr Asp Tyr Asp Thr Ala Leu Gln Ser  
820 825 830

Lys Ala Ala Glu Trp His Cys Ser Leu Arg Asp Leu Glu Phe Ser Asn  
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Asp Pro Asp Lys Ala Ala  
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Asp Ile Ser Gln Thr Ala Ala Thr Val Asp Val Ser Phe Asn Phe Phe  
35 40 45

Arg Val Leu Leu Gln Ser His Thr Lys Lys Glu Glu Trp Lys Ile Lys  
50 55 60

His Leu Asp Leu Ser Asn Asn Leu Ile Ser Lys Ile Thr Leu Ser Pro  
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Phe Ala Tyr Leu His Ala Leu Glu Val Leu Asn Leu Ser Asn Asn Ala  
85 90 95

Ile His Ser Leu Ser Leu Asp Leu Leu Ser Pro Lys Ser Ser Trp Val  
100 105 110

Lys Arg His Arg Ser Ser Phe Arg Asn Arg Phe Pro Leu Leu Lys Val  
115 120 125

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 gtggatgtaa gtttcaattt ctttagagtt ctcttacagt ctcacacgaa aaaagaagag 180  
 tggaaaataa aacatctgga cctcagtaac aatctcatat caaaaataac ctttaagccct 240  
 tttgcatatt tacatgcttt ggaagtgtta aacctcagca acaatgccat ccactccctc 300  
 tcattggatc tactcagtc ctaagtccca tgggtgaaac gccacagaag cagcttcaga 360  
 aacagggttc cattgctgaa ggtgctcatt cttcaaagaa ataaactcag tgacactccc 420  
 aagggactgt ggaactgaa gtcattgcag agtttgatc tgtcattcaa tgggatattg 480  
 caaatagggt ggtctgattt tcacaactgc ctgcaactgg agaattctctg tttaaagagc 540  
 aacaagatat tcaaaattcc ccacaagcc ttcaaggacc tcaaaaaatt acagggtcata 600  
 gaccttagca acaatgctct gattaccatc ctaccaatga tgatcatagc tctagaattt 660  
 ccccatctag tgggtgactt ggctgataat aactggcagt gtgatgatag tgtggcagtc 720  
 tttcaaaatt ttatttctga atcctggagg aaaaagtggg atgtcatttg caacagggtct 780  
 atagggagtg aggaggccaa cgggggcaact cccagagca ggatttccag ggaaacccgc 840  
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 cagggaggaa ggcacacggg catttctact ctggggaaga aggcaaaggc cggctctggt 960  
 ctcaggaaga agcagagacg gctgccaaag agtggttagaa gcaccgcga tgtgcaggct 1020  
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 atcacattcc ttgtgcctt cagcctgggg gctttcaca ggccttatgt tgacagactg 1140  
 tggcaaaaaa agtgccagag caaaagccct ggcctggaca acgcgtattc aaacgagggc 1200  
 ttctacgatg acatggaagc tgcggggcac acaccacacc cagagaccca tctgcgcca 1260  
 gtatttctct atctaagcct ctacgagaac cagaccctt tctgggtgac acagccacac 1320  
 ccacacgcca ccgtaattcc tgatagaact ctgggaagga gcagaaagga tcctggcagt 1380  
 tcgcagagcc caggacagt cggggacaac accggggcag gaagtggaaa tgatggtgca 1440  
 gtctattcca ttctccagag acatccacat gccggttaac gtgaactaat gtcagcagcg 1500  
 caggaccaca tccataggaa tgatattctc ggagaatgga cttatgaaac tgtggcccag 1560  
 gaagagcctc tcagtgcaca ttcagtgggc gtctctcttg tagctggcac gtctcacgct 1620  
 gtctctggct caagccgtta tgattccaat gaattagacc cttccctctc cggagaaata 1680  
 acagcttccc tctgtaaaat gctaacacat gcagaagcac agaggactgg agatagtaag 1740  
 gaaagagggg gcaactgaaca gtcacttttg gactgcgaga tgggaattttc taaggaaagg 1800  
 caagtgaagt catccattga tttgctgagc atacagcagc caaggctgtc cggggcaagg 1860  
 gctgaggaag cgctttcagc ccactacagc gaggttccat acggtgacct aagagacaca 1920  
 ggcccatcag tctttctctc aagatgggac agtggcctgg atgtcactcc tgctaacaag 1980  
 gaaccagtgc agaaatccac tccttctgac acttgctgtg agttggagag tgactgtgac 2040  
 tctgatgagg ggtctctgtt cactctgagc tccataagtt cagagagtgc aaggagcaag 2100  
 actgaagagg cagtgcctga tgaggagtcc ctgcaggacg agagctcagg ggcaagcaag 2160  
 gacaatgtga cggctgtaga cagtcttgag gaaaatgtta ccttccaaac aattccaggg 2220  
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 atgtacaaga ctcatctgga aaatgcctct gacactgata gatctgaggg cctgtcacc 2340  
 tggcccaggt caccagggaa tagtccctta ggggatgagt ttccgggcat gttcacttat 2400  
 gattatgaca cagctcttca atccaaggca gcagaatggc attgctcact tagagactta 2460  
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 gatcctgata aggtcgcc 2538

<210> 14  
 <211> 846  
 <212> PRT  
 <213> Homo sapiens

<400> 14  
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 Asp Ile Ser Gln Thr Ala Ala Thr Val Asp Val Ser Phe Asn Phe Phe  
 35 40 45  
 Arg Val Leu Leu Gln Ser His Thr Lys Lys Glu Glu Trp Lys Ile Lys  
 50 55 60  
 His Leu Asp Leu Ser Asn Asn Leu Ile Ser Lys Ile Thr Leu Ser Pro  
 65 70 75 80  
 Phe Ala Tyr Leu His Ala Leu Glu Val Leu Asn Leu Ser Asn Asn Ala  
 85 90 95  
 Ile His Ser Leu Ser Leu Asp Leu Leu Ser Pro Lys Ser Ser Trp Val  
 100 105 110  
 Lys Arg His Arg Ser Ser Phe Arg Asn Arg Phe Pro Leu Leu Lys Val  
 115 120 125  
 Leu Ile Leu Gln Arg Asn Lys Leu Ser Asp Thr Pro Lys Gly Leu Trp  
 130 135 140  
 Lys Leu Lys Ser Leu Gln Ser Leu Asp Leu Ser Phe Asn Gly Ile Leu  
 145 150 155 160  
 Gln Ile Gly Trp Ser Asp Phe His Asn Cys Leu Gln Leu Glu Asn Leu  
 165 170 175  
 Cys Leu Lys Ser Asn Lys Ile Phe Lys Ile Pro Pro Gln Ala Phe Lys  
 180 185 190  
 Asp Leu Lys Lys Leu Gln Val Ile Asp Leu Ser Asn Asn Ala Leu Ile  
 195 200 205  
 Thr Ile Leu Pro Met Met Ile Ile Ala Leu Glu Phe Pro His Leu Val  
 210 215 220  
 Val Asp Leu Ala Asp Asn Asn Trp Gln Cys Asp Asp Ser Val Ala Val  
 225 230 235 240  
 Phe Gln Asn Phe Ile Ser Glu Ser Trp Arg Lys Lys Trp Asn Val Ile  
 245 250 255  
 Cys Asn Arg Ser Ile Gly Ser Glu Glu Ala Asn Gly Gly Thr Pro Gln  
 260 265 270  
 Ser Arg Ile Ser Arg Glu Thr Arg Leu Pro Pro Ile His Leu His Arg  
 275 280 285  
 Met Lys Ser Leu Ile Arg Ser Lys Ala Glu Arg Pro Gln Gly Gly Arg  
 290 295 300  
 His Thr Gly Ile Ser Thr Leu Gly Lys Lys Ala Lys Ala Gly Ser Gly  
 305 310 315 320  
 Leu Arg Lys Lys Gln Arg Arg Leu Pro Arg Ser Val Arg Ser Thr Arg  
 325 330 335

Asp Val Gln Ala Ala Gly Lys Lys Glu Asp Ala Pro Gln Asp Leu Ala  
 340 345 350  
 Leu Ala Val Cys Leu Ser Val Phe Ile Thr Phe Leu Val Ala Phe Ser  
 355 360 365  
 Leu Gly Ala Phe Thr Arg Pro Tyr Val Asp Arg Leu Trp Gln Lys Lys  
 370 375 380  
 Cys Gln Ser Lys Ser Pro Gly Leu Asp Asn Ala Tyr Ser Asn Glu Gly  
 385 390 395 400  
 Phe Tyr Asp Asp Met Glu Ala Ala Gly His Thr Pro His Pro Glu Thr  
 405 410 415  
 His Leu Arg Gln Val Phe Pro His Leu Ser Leu Tyr Glu Asn Gln Thr  
 420 425 430  
 Pro Phe Trp Val Thr Gln Pro His Pro His Ala Thr Val Ile Pro Asp  
 435 440 445  
 Arg Thr Leu Gly Arg Ser Arg Lys Asp Pro Gly Ser Ser Gln Ser Pro  
 450 455 460  
 Gly Gln Cys Gly Asp Asn Thr Gly Ala Gly Ser Gly Asn Asp Gly Ala  
 465 470 475 480  
 Val Tyr Ser Ile Leu Gln Arg His Pro His Ala Gly Asn Arg Glu Leu  
 485 490 495  
 Met Ser Ala Ala Gln Asp His Ile His Arg Asn Asp Ile Leu Gly Glu  
 500 505 510  
 Trp Thr Tyr Glu Thr Val Ala Gln Glu Glu Pro Leu Ser Ala His Ser  
 515 520 525  
 Val Gly Val Ser Ser Val Ala Gly Thr Ser His Ala Val Ser Gly Ser  
 530 535 540  
 Ser Arg Tyr Asp Ser Asn Glu Leu Asp Pro Ser Leu Ser Gly Glu Ile  
 545 550 555 560  
 Thr Ala Ser Leu Cys Lys Met Leu Thr His Ala Glu Ala Gln Arg Thr  
 565 570 575  
 Gly Asp Ser Lys Glu Arg Gly Gly Thr Glu Gln Ser Leu Trp Asp Ser  
 580 585 590  
 Gln Met Glu Phe Ser Lys Glu Arg Gln Val Ser Ser Ser Ile Asp Leu  
 595 600 605  
 Leu Ser Ile Gln Gln Pro Arg Leu Ser Gly Ala Arg Ala Glu Glu Ala  
 610 615 620  
 Leu Ser Ala His Tyr Ser Glu Val Pro Tyr Gly Asp Pro Arg Asp Thr  
 625 630 635 640  
 Gly Pro Ser Val Phe Pro Pro Arg Trp Asp Ser Gly Leu Asp Val Thr  
 645 650 655  
 Pro Ala Asn Lys Glu Pro Val Gln Lys Ser Thr Pro Ser Asp Thr Cys

660	665	670	
Cys Glu Leu Glu Ser Asp Cys Asp Ser Asp Glu Gly Ser Leu Phe Thr			
675	680	685	
Leu Ser Ser Ile Ser Ser Glu Ser Ala Arg Ser Lys Thr Glu Glu Ala			
690	695	700	
Val Pro Asp Glu Glu Ser Leu Gln Asp Glu Ser Ser Gly Ala Ser Lys			
705	710	715	720
Asp Asn Val Thr Ala Val Asp Ser Leu Glu Glu Asn Val Thr Phe Gln			
725	730		735
Thr Ile Pro Gly Lys Cys Lys Asn Gln Glu Asp Pro Phe Glu Lys Pro			
740	745	750	
Leu Ile Ser Ala Pro Asp Ser Gly Met Tyr Lys Thr His Leu Glu Asn			
755	760	765	
Ala Ser Asp Thr Asp Arg Ser Glu Gly Leu Ser Pro Trp Pro Arg Ser			
770	775	780	
Pro Gly Asn Ser Pro Leu Gly Asp Glu Phe Pro Gly Met Phe Thr Tyr			
785	790	795	800
Asp Tyr Asp Thr Ala Leu Gln Ser Lys Ala Ala Glu Trp His Cys Ser			
805	810		815
Leu Arg Asp Leu Glu Phe Ser Asn Val Asp Val Leu Gln Gln Thr Pro			
820	825		830
Pro Cys Ser Ala Glu Val Pro Ser Asp Pro Asp Lys Ala Ala			
835	840	845	

<210> 15  
 <211> 1089  
 <212> DNA  
 <213> Homo sapiens

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 tatattctga caaattgttc ttttaccgga aagtgtgata tacctgtgga catatcacag 180  
 acagcagcca ctgtggatgt aagtttcaat ttcttttagag ttctcttaca gtctcacacg 240  
 aaaaaagaag agtggaaaat aaaacatctg gacctcagta acaatctcat atcaaaaata 300  
 accttaagcc cttttgcata ttacatgct ttggaagtgt taaacctcag caacaatgcc 360  
 atccactccc tctcattgga tctactcagt cctaagtcct catgggtgaa acgccacaga 420  
 agcagcttca gaaacaggtt tccattgctg aagggtgctca ttcttcaaag aaataaactc 480  
 agtgacactc ccaagggact gtggaaactg aagtcattgc agagtttgga tctgtcattc 540  
 aatgggatat tgcaaatagg gtggtctgat tttcacaact gcctgcaact ggagaatctc 600  
 tgttttaaaga gcaacaagat attcaaaatt cccccacaag cttcaagga cctcaaaaaa 660  
 ttacaggtca tagaccttag caacaatgct ctgattacca tcctaccaat gatgatcata 720  
 gctctagaat ttcccatct agtggttgac ttggctgata ataactggca gtgtgatgat 780  
 agtgtggcag tctttcaaaa ttttatttct gaatcctgga ggaaaaagtg gaatgtcatt 840  
 tgcaacaggt ctataggagg tgaggaggcc aacgggggca ctccccagag caggatttcc 900  
 agggaaaccc gccttcctcc cattcatctg catcgcatga aaagcctcat aaggagcaaa 960  
 gcagagaggc cccaggagg aaggcacacg ggcatttcta ctctggggaa gaaggcaaag 1020  
 gccggctctg gtctcaggaa gaagcagaga cggctgccaa ggagtgttag aagcaccgcg 1080  
 gatgtgcag 1089

<210> 16  
 <211> 363  
 <212> PRT  
 <213> Homo sapiens

<400> 16  
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 Phe Thr Gly Ile Met Thr Asn Ala Ser Arg Lys Ser Asn Ile Leu Phe  
 20 25 30  
 Asn Ser Glu Cys Gln Trp Asn Glu Tyr Ile Leu Thr Asn Cys Ser Phe  
 35 40 45  
 Thr Gly Lys Cys Asp Ile Pro Val Asp Ile Ser Gln Thr Ala Ala Thr  
 50 55 60  
 Val Asp Val Ser Phe Asn Phe Phe Arg Val Leu Leu Gln Ser His Thr  
 65 70 75 80  
 Lys Lys Glu Glu Trp Lys Ile Lys His Leu Asp Leu Ser Asn Asn Leu  
 85 90 95  
 Ile Ser Lys Ile Thr Leu Ser Pro Phe Ala Tyr Leu His Ala Leu Glu  
 100 105 110  
 Val Leu Asn Leu Ser Asn Asn Ala Ile His Ser Leu Ser Leu Asp Leu  
 115 120 125  
 Leu Ser Pro Lys Ser Ser Trp Val Lys Arg His Arg Ser Ser Phe Arg  
 130 135 140  
 Asn Arg Phe Pro Leu Leu Lys Val Leu Ile Leu Gln Arg Asn Lys Leu  
 145 150 155 160  
 Ser Asp Thr Pro Lys Gly Leu Trp Lys Leu Lys Ser Leu Gln Ser Leu  
 165 170 175  
 Asp Leu Ser Phe Asn Gly Ile Leu Gln Ile Gly Trp Ser Asp Phe His  
 180 185 190  
 Asn Cys Leu Gln Leu Glu Asn Leu Cys Leu Lys Ser Asn Lys Ile Phe  
 195 200 205  
 Lys Ile Pro Pro Gln Ala Phe Lys Asp Leu Lys Lys Leu Gln Val Ile  
 210 215 220  
 Asp Leu Ser Asn Asn Ala Leu Ile Thr Ile Leu Pro Met Met Ile Ile  
 225 230 235 240  
 Ala Leu Glu Phe Pro His Leu Val Val Asp Leu Ala Asp Asn Asn Trp  
 245 250 255  
 Gln Cys Asp Asp Ser Val Ala Val Phe Gln Asn Phe Ile Ser Glu Ser  
 260 265 270  
 Trp Arg Lys Lys Trp Asn Val Ile Cys Asn Arg Ser Ile Gly Ser Glu  
 275 280 285  
 Glu Ala Asn Gly Gly Thr Pro Gln Ser Arg Ile Ser Arg Glu Thr Arg

290 295 300  
 Leu Pro Pro Ile His Leu His Arg Met Lys Ser Leu Ile Arg Ser Lys  
 305 310 315 320  
 Ala Glu Arg Pro Gln Gly Gly Arg His Thr Gly Ile Ser Thr Leu Gly  
 325 330 335  
 Lys Lys Ala Lys Ala Gly Ser Gly Leu Arg Lys Lys Gln Arg Arg Leu  
 340 345 350  
 Pro Arg Ser Val Arg Ser Thr Arg Asp Val Gln  
 355 360  
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 <211> 729  
 <212> DNA  
 <213> Homo sapiens  
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 tatattctga caaattgttc ttttaccgga aagtgtgata tacctgtgga catatcacag 180  
 acagcagcca ctgtggatgt aagtttcaat ttcttttagag ttctcttaca gtctcacacg 240  
 aaaaaagaag agtggaaaaat aaaacatctg gacctcagta acaatctcat atcaaaaata 300  
 accttaagcc cttttgcata tttacatgct ttggaagtgt taaacctcag caacaatgcc 360  
 atccactccc tctcattgga tctactcagt cctaagtcct catgggtgaa acgccacaga 420  
 agcagcttca gaaacagggtt tccattgctg aagggtgctca ttcttcaaag aaataaactc 480  
 agtgacactc ccaaggggag tgaggaggcc aacgggggca ctccccagag caggatttcc 540  
 agggaaaccc gccttcctcc cattcatctg catcgcatga aaagcctcat aaggagcaaa 600  
 gcagagaggc cccagggagg aaggcacacg ggcatttcta ctctggggaa gaaggcaaag 660  
 gccggctctg gtctcaggaa gaagcagaga cggctgccaa ggagtgttag aagcacccgc 720  
 gatgtgcag 729  
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 <211> 243  
 <212> PRT  
 <213> Homo sapiens  
 <400> 18  
 Met Lys Asn Leu Tyr Phe Arg Val Ile Thr Ile Val Ile Gly Leu Tyr  
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 Phe Thr Gly Ile Met Thr Asn Ala Ser Arg Lys Ser Asn Ile Leu Phe  
 20 25 30  
 Asn Ser Glu Cys Gln Trp Asn Glu Tyr Ile Leu Thr Asn Cys Ser Phe  
 35 40 45  
 Thr Gly Lys Cys Asp Ile Pro Val Asp Ile Ser Gln Thr Ala Ala Thr  
 50 55 60  
 Val Asp Val Ser Phe Asn Phe Phe Arg Val Leu Leu Gln Ser His Thr  
 65 70 75 80  
 Lys Lys Glu Glu Trp Lys Ile Lys His Leu Asp Leu Ser Asn Asn Leu  
 85 90 95  
 Ile Ser Lys Ile Thr Leu Ser Pro Phe Ala Tyr Leu His Ala Leu Glu  
 100 105 110

Val Leu Asn Leu Ser Asn Asn Ala Ile His Ser Leu Ser Leu Asp Leu  
 115 120 125

Leu Ser Pro Lys Ser Ser Trp Val Lys Arg His Arg Ser Ser Phe Arg  
 130 135 140

Asn Arg Phe Pro Leu Leu Lys Val Leu Ile Leu Gln Arg Asn Lys Leu  
 145 150 155 160

Ser Asp Thr Pro Lys Gly Ser Glu Glu Ala Asn Gly Gly Thr Pro Gln  
 165 170 175

Ser Arg Ile Ser Arg Glu Thr Arg Leu Pro Pro Ile His Leu His Arg  
 180 185 190

Met Lys Ser Leu Ile Arg Ser Lys Ala Glu Arg Pro Gln Gly Gly Arg  
 195 200 205

His Thr Gly Ile Ser Thr Leu Gly Lys Lys Ala Lys Ala Gly Ser Gly  
 210 215 220

Leu Arg Lys Lys Gln Arg Arg Leu Pro Arg Ser Val Arg Ser Thr Arg  
 225 230 235 240

Asp Val Gln

<210> 19  
 <211> 1017  
 <212> DNA  
 <213> Homo sapiens

<400> 19  
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 aattgttctt ttaccggaaa gtgtgatata cctgtggaca tatcacagac agcagccact 120  
 gtggatgtaa gtttcaattt ctttagagtt ctcttacagt ctcacacgaa aaaagaagag 180  
 tggaaaataa aacatctgga cctcagtaac aatctcatat caaaaataac cttaagccct 240  
 tttgcatatt tacatgcttt ggaagtgtta aacctcagca acaatgccat ccactccctc 300  
 tcattggatc tactcagtc taagtcctca tgggtgaaac gccacagaag cagcttcaga 360  
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 aagggactgt ggaaactgaa gtcattgcag agtttgatc tgtcattcaa tgggatattg 480  
 caaatagggt ggtctgattt tcacaactgc ctgcaactgg agaattctctg tttaaagagc 540  
 aacaagatat tcaaaattcc cccacaagcc ttcaaggacc tcaaaaaatt acaggtcata 600  
 gaccttagca acaatgctct gattaccatc ctaccaatga tgatcatagc tctagaattt 660  
 ccccatctag tggttgactt ggctgataat aactggcagt gtgatgatag tgtggcagtc 720  
 tttcaaaatt ttatttctga atcctggagg aaaaagtgga atgtcatttg caacaggtct 780  
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 cttcctccca ttcactgca tcgcatgaaa agcctcataa ggagcaaagc agagaggccc 900  
 cagggaggaa ggcacacggg catttctact ctggggaaga aggcaaagc cggctctggt 960  
 ctcaggaaga agcagagacg gctgccaagg agtgtagaa gcacccgcga tgtgcag 1017

<210> 20  
 <211> 339  
 <212> PRT  
 <213> Homo sapiens

<400> 20  
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Tyr Ile Leu Thr Asn Cys Ser Phe Thr Gly Lys Cys Asp Ile Pro Val



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Asp	Ile	Ser	Gln	Thr	Ala	Ala	Thr	Val	Asp	Val	Ser	Phe	Asn	Phe	Phe
		35					40					45			
Arg	Val	Leu	Leu	Gln	Ser	His	Thr	Lys	Lys	Glu	Glu	Trp	Lys	Ile	Lys
		50				55					60				
His	Leu	Asp	Leu	Ser	Asn	Asn	Leu	Ile	Ser	Lys	Ile	Thr	Leu	Ser	Pro
						70					75				80
Phe	Ala	Tyr	Leu	His	Ala	Leu	Glu	Val	Leu	Asn	Leu	Ser	Asn	Asn	Ala
				85					90					95	
Ile	His	Ser	Leu	Ser	Leu	Asp	Leu	Leu	Ser	Pro	Lys	Ser	Ser	Trp	Val
			100					105					110		
Lys	Arg	His	Arg	Ser	Ser	Phe	Arg	Asn	Arg	Phe	Pro	Leu	Leu	Lys	Val
		115					120					125			
Leu	Ile	Leu	Gln	Arg	Asn	Lys	Leu	Ser	Asp	Thr	Pro	Lys	Gly	Leu	Trp
		130				135					140				
Lys	Leu	Lys	Ser	Leu	Gln	Ser	Leu	Asp	Leu	Ser	Phe	Asn	Gly	Ile	Leu
						150					155				160
Gln	Ile	Gly	Trp	Ser	Asp	Phe	His	Asn	Cys	Leu	Gln	Leu	Glu	Asn	Leu
				165					170					175	
Cys	Leu	Lys	Ser	Asn	Lys	Ile	Phe	Lys	Ile	Pro	Pro	Gln	Ala	Phe	Lys
			180					185					190		
Asp	Leu	Lys	Lys	Leu	Gln	Val	Ile	Asp	Leu	Ser	Asn	Asn	Ala	Leu	Ile
		195					200					205			
Thr	Ile	Leu	Pro	Met	Met	Ile	Ile	Ala	Leu	Glu	Phe	Pro	His	Leu	Val
		210				215					220				
Val	Asp	Leu	Ala	Asp	Asn	Asn	Trp	Gln	Cys	Asp	Asp	Ser	Val	Ala	Val
						230					235				240
Phe	Gln	Asn	Phe	Ile	Ser	Glu	Ser	Trp	Arg	Lys	Lys	Trp	Asn	Val	Ile
				245					250					255	
Cys	Asn	Arg	Ser	Ile	Gly	Ser	Glu	Glu	Ala	Asn	Gly	Gly	Thr	Pro	Gln
			260					265					270		
Ser	Arg	Ile	Ser	Arg	Glu	Thr	Arg	Leu	Pro	Pro	Ile	His	Leu	His	Arg
		275					280					285			
Met	Lys	Ser	Leu	Ile	Arg	Ser	Lys	Ala	Glu	Arg	Pro	Gln	Gly	Gly	Arg
		290				295					300				
His	Thr	Gly	Ile	Ser	Thr	Leu	Gly	Lys	Lys	Ala	Lys	Ala	Gly	Ser	Gly
						310					315				320
Leu	Arg	Lys	Lys	Gln	Arg	Arg	Leu	Pro	Arg	Ser	Val	Arg	Ser	Thr	Arg
				325					330					335	
Asp	Val	Gln													

<210> 21  
 <211> 657  
 <212> DNA  
 <213> Homo sapiens

<400> 21  
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 tggaaaataa aacatctgga cctcagtaac aatctcatat caaaaataac cttaagccct 240  
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 tcattggatc tactcagtcc taagtcctca tgggtgaaac gccacagaag cagcttcaga 360  
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 cttcctccca ttcatctgca tcgcatgaaa agcctcataa ggagcaaagc agagaggccc 540  
 cagggaggaa ggcacacggg catttctact ctggggaaga aggcaaaggc cggctctggt 600  
 ctcaggaaga agcagagacg gctgccaaag agtgttagaa gcacccgcga tgtgcag 657

<210> 22  
 <211> 219  
 <212> PRT  
 <213> Homo sapiens

<400> 22  
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 Tyr Ile Leu Thr Asn Cys Ser Phe Thr Gly Lys Cys Asp Ile Pro Val  
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 Asp Ile Ser Gln Thr Ala Ala Thr Val Asp Val Ser Phe Asn Phe Phe  
 35 40 45  
 Arg Val Leu Leu Gln Ser His Thr Lys Lys Glu Glu Trp Lys Ile Lys  
 50 55 60  
 His Leu Asp Leu Ser Asn Asn Leu Ile Ser Lys Ile Thr Leu Ser Pro  
 65 70 75 80  
 Phe Ala Tyr Leu His Ala Leu Glu Val Leu Asn Leu Ser Asn Asn Ala  
 85 90 95  
 Ile His Ser Leu Ser Leu Asp Leu Leu Ser Pro Lys Ser Ser Trp Val  
 100 105 110  
 Lys Arg His Arg Ser Ser Phe Arg Asn Arg Phe Pro Leu Leu Lys Val  
 115 120 125  
 Leu Ile Leu Gln Arg Asn Lys Leu Ser Asp Thr Pro Lys Gly Ser Glu  
 130 135 140  
 Glu Ala Asn Gly Gly Thr Pro Gln Ser Arg Ile Ser Arg Glu Thr Arg  
 145 150 155 160  
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 Ala Glu Arg Pro Gln Gly Gly Arg His Thr Gly Ile Ser Thr Leu Gly  
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 Lys Lys Glu Glu Trp Lys Ile Lys His Leu Asp Leu Ser Asn Asn Leu  
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 130 135 140  
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 Pro His Ala Thr Val Ile Pro Asp Arg Thr Leu Gly Arg Ser Arg Lys  
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 Asp Pro Gly Ser Ser Gln Ser Pro Gly Gln Cys Gly Asp Asn Thr Gly  
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&lt;211&gt; 852

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

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Leu Ile Ser Ala Pro Asp Ser Gly Met Tyr Lys Thr His Leu Glu Asn  
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Pro Gly Asn Ser Pro Leu Gly Asp Glu Phe Pro Gly Met Phe Thr Tyr  
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Asp Tyr Asp Thr Ala Leu Gln Ser Lys Ala Ala Glu Trp His Cys Ser  
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Phe Thr Gly Ile Met Thr Asn Ala Ser Arg Lys Ser Asn Ile Leu Phe
          20          25          30

Asn Ser Glu Cys Gln Trp Asn Glu Tyr Ile Leu Thr Asn Cys Ser Phe
          35          40          45

Thr Gly Lys Cys Asp Ile Pro Val Asp Ile Ser Gln Thr Ala Ala Thr
          50          55          60

Val Asp Val Ser Phe Asn Phe Phe Arg Val Leu Leu Gln Ser His Thr
65          70          75          80

Lys Lys Glu Glu Trp Lys Ile Lys His Leu Asp Leu Ser Asn Asn Leu
          85          90          95

Ile Ser Lys Ile Thr Leu Ser Pro Phe Ala Tyr Leu His Ala Leu Glu
          100          105          110

Val Leu Asn Leu Ser Asn Asn Ala Ile His Ser Leu Ser Leu Asp Leu
          115          120          125

Leu Ser Pro Lys Ser Ser Trp Val Lys Arg His Arg Ser Ser Phe Arg
          130          135          140

Asn Arg Phe Pro Leu Leu Lys Val Leu Ile Leu Gln Arg Asn Lys Leu
145          150          155          160

Ser Asp Thr Pro Lys Gly Leu Trp Lys Leu Lys Ser Leu Gln Ser Leu
          165          170          175

Asp Leu Ser Phe Asn Gly Ile Leu Gln Ile Gly Trp Ser Asp Phe His
          180          185          190

Asn Cys Leu Gln Leu Glu Asn Leu Cys Leu Lys Ser Asn Lys Ile Phe
          195          200          205

Lys Ile Pro Pro Gln Ala Phe Lys Asp Leu Lys Lys Leu Gln Val Ile
          210          215          220

Asp Leu Ser Asn Asn Ala Leu Ile Thr Ile Leu Pro Met Met Ile Ile
225          230          235          240

Ala Leu Glu Phe Pro His Leu Val Val Asp Leu Ala Asp Asn Asn Trp
          245          250          255

Gln Cys Asp Asp Ser Val Ala Val Phe Gln Asn Phe Ile Ser Glu Ser
          260          265          270

Trp Arg Lys Lys Trp Asn Val Ile Cys Asn Arg Ser Ile Gly Ser Glu
          275          280          285

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Glu Ala Asn Gly Gly Thr Pro Gln Ser Arg Ile Ser Arg Glu Thr Arg  
 290 295 300

Leu Pro Pro Ile His Leu His Arg Met Lys Ser Leu Ile Arg Ser Lys  
 305 310 315 320

Ala Glu Arg Pro Gln Gly Gly Arg His Thr Gly Ile Ser Thr Leu Gly  
 325 330 335

Lys Lys Ala Lys Ala Gly Ser Gly Leu Arg Lys Lys Gln Arg Arg Leu  
 340 345 350

Pro Arg Ser Val Arg Ser Thr Arg Asp Val Gln His His His His His  
 355 360 365

His

<210> 29  
 <211> 747  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> histidine tagged INSP179-EC-SV1 nucleotide sequence

<400> 29  
 atgaaaaacc tctatttcag agtcattacc atagttatag gtctttatatt tactggaata 60  
 atgacaaatg catcaagaaa aagcaatatt ttattcaatt ctgaatgcca atggaatgaa 120  
 tatattctga caaattgttc ttttaccgga aagtgtgata tacctgtgga catatcacag 180  
 acagcagcca ctgtggatgt aagtttcaat ttcttttagag ttctcttaca gtctcacacg 240  
 aaaaaagaag agtggaaaat aaaacatctg gacctcagta acaatctcat atcaaaaata 300  
 accttaagcc cttttgcata tttacatgct ttggaagtgt taaacctcag caacaatgcc 360  
 atccactccc tctcattgga tctactcagt cctaagtcct catgggtgaa acgccacaga 420  
 agcagcttca gaaacagggt tccattgctg aaggtgctca ttcttcaaag aaataaactc 480  
 agtgacactc ccaaggggag tgaggaggcc aacgggggca ctccccagag caggatttcc 540  
 agggaaaccc gccttcctcc cattcatctg catcgcatga aaagcctcat aaggagcaaa 600  
 gcagagaggc cccagggagg aaggcacacg ggcatttcta ctctggggaa gaaggcaaag 660  
 gccggctctg gtctcaggaa gaagcagaga cggctgccaa ggagtgttag aagcaccgcg 720  
 gatgtgcagc accatcacca tcaccat 747

<210> 30  
 <211> 249  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> histidine tagged INSP179-EC-SV1 polypeptide sequence

<400> 30  
 Met Lys Asn Leu Tyr Phe Arg Val Ile Thr Ile Val Ile Gly Leu Tyr  
 1 5 10 15

Phe Thr Gly Ile Met Thr Asn Ala Ser Arg Lys Ser Asn Ile Leu Phe  
 20 25 30

Asn Ser Glu Cys Gln Trp Asn Glu Tyr Ile Leu Thr Asn Cys Ser Phe  
 35 40 45

Thr Gly Lys Cys Asp Ile Pro Val Asp Ile Ser Gln Thr Ala Ala Thr

50		55		60
Val Asp Val Ser Phe Asn Phe Phe Arg Val Leu Leu Gln Ser His Thr				
65		70		75
Lys Lys Glu Glu Trp Lys Ile Lys His Leu Asp Leu Ser Asn Asn Leu				
	85		90	95
Ile Ser Lys Ile Thr Leu Ser Pro Phe Ala Tyr Leu His Ala Leu Glu				
	100		105	110
Val Leu Asn Leu Ser Asn Asn Ala Ile His Ser Leu Ser Leu Asp Leu				
	115		120	125
Leu Ser Pro Lys Ser Ser Trp Val Lys Arg His Arg Ser Ser Phe Arg				
	130		135	140
Asn Arg Phe Pro Leu Leu Lys Val Leu Ile Leu Gln Arg Asn Lys Leu				
145		150		155
Ser Asp Thr Pro Lys Gly Ser Glu Glu Ala Asn Gly Gly Thr Pro Gln				
	165		170	175
Ser Arg Ile Ser Arg Glu Thr Arg Leu Pro Pro Ile His Leu His Arg				
	180		185	190
Met Lys Ser Leu Ile Arg Ser Lys Ala Glu Arg Pro Gln Gly Gly Arg				
	195		200	205
His Thr Gly Ile Ser Thr Leu Gly Lys Lys Ala Lys Ala Gly Ser Gly				
	210		215	220
Leu Arg Lys Lys Gln Arg Arg Leu Pro Arg Ser Val Arg Ser Thr Arg				
225		230		235
Asp Val Gln His His His His His His				
	245			

&lt;210&gt; 31

&lt;211&gt; 1035

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; histidine tagged INSP179-EC mature nucleotide sequence

&lt;400&gt; 31

tcaagaaaaa	gcaatatattt	attcaattct	gaatgccaat	ggaatgaata	tattctgaca	60
aattgttctt	ttaccggaaa	gtgtgatata	cctgtggaca	tatcacagac	agcagccact	120
gtggatgtaa	gtttcaattt	ctttagagtt	ctcttacagt	ctcacacgaa	aaaagaagag	180
tggaaaataa	aacatctgga	cctcagtaac	aatctcatat	caaaaataac	cttaagccct	240
tttgcataat	tacatgcttt	ggaagtgtta	aacctcagca	acaatgccat	ccactccctc	300
tcattggatc	tactcagtc	taagtccctca	tgggtgaaac	gccacagaag	cagcttcaga	360
aacaggtttc	cattgctgaa	ggtgctcatt	cttcaaagaa	ataaactcag	tgacactccc	420
aagggactgt	ggaaactgaa	gtcattgcag	agtttggatc	tgtcattcaa	tgggatattg	480
caaatagggt	ggtctgattt	tcacaactgc	ctgcaactgg	agaatctctg	tttaaagagc	540
aacaagatat	tcaaaattcc	cccacaagcc	ttcaaggacc	tcaaaaaatt	acaggtcata	600
gaccttagca	acaatgctct	gattaccatc	ctaccaatga	tgatcatagc	tctagaattt	660
ccccatctag	tggttgactt	ggctgataat	aactggcagt	gtgatgatag	tgtggcagtc	720
tttcaaaatt	ttatttctga	atcctggagg	aaaaagtgga	atgtcatttg	caacagggtc	780
atagggagtg	aggaggccaa	cggggggcact	cccagagca	ggatttccag	ggaaaccgcg	840

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cttcctccca ttcatctgca tcgcatgaaa agcctcataa ggagcaaagc agagaggccc 900
caggaggaggaa ggcacacggg catttctact ctggggaaga aggcaaaggc cggctctggt 960
ctcaggaaga agcagagacg gctgccaagg agtgtttagaa gcacccgcga tgtgcagcac 1020
catcaccatc accat 1035

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<210> 32  
 <211> 345  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> histidine tagged INSP179-EC mature polypeptide sequence

<400> 32  
 Ser Arg Lys Ser Asn Ile Leu Phe Asn Ser Glu Cys Gln Trp Asn Glu  
 1 5 10 15  
 Tyr Ile Leu Thr Asn Cys Ser Phe Thr Gly Lys Cys Asp Ile Pro Val  
 20 25 30  
 Asp Ile Ser Gln Thr Ala Ala Thr Val Asp Val Ser Phe Asn Phe Phe  
 35 40 45  
 Arg Val Leu Leu Gln Ser His Thr Lys Lys Glu Glu Trp Lys Ile Lys  
 50 55 60  
 His Leu Asp Leu Ser Asn Asn Leu Ile Ser Lys Ile Thr Leu Ser Pro  
 65 70 75 80  
 Phe Ala Tyr Leu His Ala Leu Glu Val Leu Asn Leu Ser Asn Asn Ala  
 85 90 95  
 Ile His Ser Leu Ser Leu Asp Leu Leu Ser Pro Lys Ser Ser Trp Val  
 100 105 110  
 Lys Arg His Arg Ser Ser Phe Arg Asn Arg Phe Pro Leu Leu Lys Val  
 115 120 125  
 Leu Ile Leu Gln Arg Asn Lys Leu Ser Asp Thr Pro Lys Gly Leu Trp  
 130 135 140  
 Lys Leu Lys Ser Leu Gln Ser Leu Asp Leu Ser Phe Asn Gly Ile Leu  
 145 150 155 160  
 Gln Ile Gly Trp Ser Asp Phe His Asn Cys Leu Gln Leu Glu Asn Leu  
 165 170 175  
 Cys Leu Lys Ser Asn Lys Ile Phe Lys Ile Pro Pro Gln Ala Phe Lys  
 180 185 190  
 Asp Leu Lys Lys Leu Gln Val Ile Asp Leu Ser Asn Asn Ala Leu Ile  
 195 200 205  
 Thr Ile Leu Pro Met Met Ile Ile Ala Leu Glu Phe Pro His Leu Val  
 210 215 220  
 Val Asp Leu Ala Asp Asn Asn Trp Gln Cys Asp Asp Ser Val Ala Val  
 225 230 235 240  
 Phe Gln Asn Phe Ile Ser Glu Ser Trp Arg Lys Lys Trp Asn Val Ile  
 245 250 255

Cys Asn Arg Ser Ile Gly Ser Glu Glu Ala Asn Gly Gly Thr Pro Gln  
260 265 270

Ser Arg Ile Ser Arg Glu Thr Arg Leu Pro Pro Ile His Leu His Arg  
275 280 285

Met Lys Ser Leu Ile Arg Ser Lys Ala Glu Arg Pro Gln Gly Gly Arg  
290 295 300

His Thr Gly Ile Ser Thr Leu Gly Lys Lys Ala Lys Ala Gly Ser Gly  
305 310 315 320

Leu Arg Lys Lys Gln Arg Arg Leu Pro Arg Ser Val Arg Ser Thr Arg  
325 330 335

Asp Val Gln His His His His His His  
340 345

<210> 33  
<211> 675  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> histidine tagged INSP179-EC-SV1 mature nucleotide sequence

<400> 33  
tcaagaaaaa gcaatatattt attcaattct gaatgccaat ggaatgaata tattctgaca 60  
aattgttctt ttaccggaaa gtgtgatata cctgtggaca tatcacagac agcagccact 120  
gtggatgtaa gtttcaattt ctttagagtt ctcttacagt ctcacacgaa aaaagaagag 180  
tggaataaa aacatctgga cctcagtaac aatctcatat caaaaataac cttagccct 240  
tttgcattt tacatgcttt ggaagtgtta aacctcagca acaatgccat cactccctc 300  
tcattggatc tactcagtc taagtcctca tgggtgaaac gccacagaag cagcttcaga 360  
aacaggtttc cattgctgaa ggtgctcatt cttcaaagaa ataaactcag tgacactccc 420  
aaggggagtg aggaggocaa cggggggcact cccagagca ggatttccag ggaaaccgc 480  
cttcctccca ttcatctgca tcgcatgaaa agcctcataa ggagcaaagc agagaggccc 540  
cagggaggaa ggcacacggg catttctact ctggggaaga aggcaaaggc cggctctggt 600  
ctcaggaaga agcagagacg gctgccaagg agtgtagaa gcaccgcga tgtgcagcac 660  
catcaccatc accat 675

<210> 34  
<211> 225  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> histidine tagged INSP179-EC-SV1 mature polypeptide sequence

<400> 34  
Ser Arg Lys Ser Asn Ile Leu Phe Asn Ser Glu Cys Gln Trp Asn Glu  
1 5 10 15  
Tyr Ile Leu Thr Asn Cys Ser Phe Thr Gly Lys Cys Asp Ile Pro Val  
20 25 30  
Asp Ile Ser Gln Thr Ala Ala Thr Val Asp Val Ser Phe Asn Phe Phe  
35 40 45  
Arg Val Leu Leu Gln Ser His Thr Lys Lys Glu Glu Trp Lys Ile Lys  
50 55 60

His Leu Asp Leu Ser Asn Asn Leu Ile Ser Lys Ile Thr Leu Ser Pro  
 65 70 75 80  
 Phe Ala Tyr Leu His Ala Leu Glu Val Leu Asn Leu Ser Asn Asn Ala  
 85 90 95  
 Ile His Ser Leu Ser Leu Asp Leu Leu Ser Pro Lys Ser Ser Trp Val  
 100 105 110  
 Lys Arg His Arg Ser Ser Phe Arg Asn Arg Phe Pro Leu Leu Lys Val  
 115 120 125  
 Leu Ile Leu Gln Arg Asn Lys Leu Ser Asp Thr Pro Lys Gly Ser Glu  
 130 135 140  
 Glu Ala Asn Gly Gly Thr Pro Gln Ser Arg Ile Ser Arg Glu Thr Arg  
 145 150 155 160  
 Leu Pro Pro Ile His Leu His Arg Met Lys Ser Leu Ile Arg Ser Lys  
 165 170 175  
 Ala Glu Arg Pro Gln Gly Gly Arg His Thr Gly Ile Ser Thr Leu Gly  
 180 185 190  
 Lys Lys Ala Lys Ala Gly Ser Gly Leu Arg Lys Lys Gln Arg Arg Leu  
 195 200 205  
 Pro Arg Ser Val Arg Ser Thr Arg Asp Val Gln His His His His His  
 210 215 220

His  
225

<210> 35  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> linker sequence

<400> 35  
 Glu Phe Gly Ala Gly Leu Val Leu Gly Gly Gln Phe Met  
 1 5 10

<210> 36  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer INSP179-CP1

<400> 36  
 atgaaaaacc tctatttcag agtcattac

<210> 37  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence



<220>  
<223> Primer INSP179-CP2

<400> 37  
ctgcacatcg cgggtgcttc taac 24

<210> 38  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer INSP179EC-EX1

<400> 38  
gcaggcttcg ccaccatgaa aaacctctat ttcag 35

<210> 39  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer INSP179EC-EX2

<400> 39  
tgatggtgat ggtgctgcac atcgcggtg cttct 35

<210> 40  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer INSP179-SP1

<400> 40  
atgaaaaacc tctatttcag agtcattac 29

<210> 41  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer INSP179-SP2

<400> 41  
caagccttca aggacctcaa 20

<210> 42  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer INSP179-SP3

<400> 42  
catgcatgc agatgaatgg 20

<210> 43  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer GCP Forward

<400> 43  
ggggacaagt ttgtacaaaa aagcaggctt cgccacc 37

<210> 44  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer GCP Reverse

<400> 44  
ggggaccact ttgtacaaga aagctgggtt tcaatgggtga tggatgatggt g 51

<210> 45  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer pEAK12F

<400> 45  
gccagcttgg cacttgatgt 20

<210> 46  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer pEAK12R

<400> 46  
gatggaggtg gacgtgtcag 20

<210> 47  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer 21M13

<400> 47  
tgtaaaacga cggccagt 18

<210> 48  
<211> 18  
<212> DNA  
<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Primer M13REV

&lt;400&gt; 48

caggaaacag ctatgacc

18

&lt;210&gt; 49

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Primer T7

&lt;400&gt; 49

taatacgact cactatagg

19

&lt;210&gt; 50

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Primer T3

&lt;400&gt; 50

attaaccctc actaaagg

18